Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) Method for the identification of biomolecules in variant libraries of biomolecules comprising the steps:

a) Production of a variant library, consisting of a number of variants (B_0) of gene sequences coding for the biomolecule, and

b) Division of the variant library into a number of compartments (W_0) of a microtiter plate and a deep well plate, respectively, which is at least by a factor of ten smaller than the number of variants in the variant library (B_0) and amounts to between 10^1 and 10^4, and wherein ~~where~~ each compartment contains a partial library which contains $K_0=B_0/W_0$ variants,

c) Production of biomolecules in the compartments and testing of the biomolecules obtained in the single compartments for a specified phenotype, whereas from the observed phenotype no direct conclusions on the genotype can be made,

d) Selection of at least one compartment, which contains biomolecules fulfilling the wanted properties,

e) Division of the partial library contained in the selected compartment into further compartments, and

f) n-fold repetition of the steps c) to e) until in every compartment maximally only one variant ($K_n<=1$) of the gene sequence coding for the biomolecule is contained.

2. (Original) The method of claim 1, wherein the wanted property is a biocatalytic activity.

3. (Previously presented) The method of claim 1, wherein in step c) also an amplification of the partial library takes place in the compartments up to an number of individuals $V_0(x)$ at the point in time x per compartment, whereas the number of individuals $V_0(x)$ divided by the number of clones per compartment K_0 gives the amplification factor $F_0(x)$ per clone.

4. (Previously presented) The method of claim 1, wherein in step e) the division is carried out under dilution of the partial library by means of factor $F_0(x)$, so that in a given volume every clone contained in the compartment is statistically present up to a number $X_0 < W_1$, this volume is divided up in a number of new compartments W_1, whereas the new number of clones per compartment amounts to $K_1 = X_0 * K_0 / W_1$.

5. (Previously presented) The method of claim 1, wherein the variant library contains 103 to 10^{15} variants of the gene sequence of the biomolecule.

6. (Previously presented) The method of claim 1, wherein in step b) the variant library is divided up in 10^1 to 10^4 compartments.

7. (Previously presented) The method of claim 1, wherein in step b) the variant library is transferred into an organism before division.

8. (Previously presented) The method of claim 7, wherein in step c) the organism is amplified to a number of organisms of 10^8 to 10^9 per compartment.

9. (Previously presented) The method of claim 7, wherein the organisms also conduct the production of the biomolecules.

10. (Previously presented) The method of claim 7, wherein the partial libraries in the compartments are re-isolated from the organisms, and the production of the biomolecules is conducted by cell-free systems.

11. (Previously presented) The method of claim 3, wherein the amplification of the partial libraries and the production of the biomolecules is conducted by cell-free systems.

12. (Previously presented) The method of claim 1, wherein the variant library consists of DNA-plasmids, which contain the gene sequence coding for the biomolecule.

13. (Previously presented) The method of claim 1, wherein the variant library consists of linear nucleic acid molecules, which contain the gene sequence coding for the biomolecule.

14. (Previously presented) The method of claim 1, wherein the biomolecules are enzymes or ribozymes or other biomolecules, which exhibit a biocatalytic activity.

15. (Previously presented) The method of claim 2, wherein the test for a biocatalytic activity is conducted with a physical detection method selected from the group consisting of UVIVIS-spectroscopy, fluorescence spectroscopy and fluorescence-correlation-spectroscopy.